

INPUT SET: S25557.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

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SEQUENCE LISTING

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(1) General Information:

- (i) APPLICANT: KOSHIBA, TOMOKAZU
- (ii) TITLE OF INVENTION: ALDEHYDE OXIDASE GENE DERIVED FROM PLANT
AND UTILIZATION THEREOF
- (iii) NUMBER OF SEQUENCES: 15
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
 - (B) STREET: P.O. BOX 747
 - (C) CITY: FALLS CHURCH
 - (D) STATE: VIRGINIA
 - (E) COUNTRY: UNITED STATES OF AMERICA
 - (F) ZIP: 22040-0747
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/943,144
 - (B) FILING DATE: 03-OCT-1997
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: STEWART, RAYMOND C.
 - (B) REGISTRATION NUMBER: 21,066
 - (C) REFERENCE/DOCKET NUMBER: 2185-208P
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (703)205-8000
 - (B) TELEFAX: (703)205-8050

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4412 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

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47 (D) TOPOLOGY: linear
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 49 (ii) MOLECULE TYPE: cDNA to mRNA
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 51 (iii) HYPOTHETICAL: NO
 52
 53 (vi) ORIGINAL SOURCE:
 54 (A) ORGANISM: maize (Zea mays L.)
 55 (B) STRAIN: cultivar: Golden Cross Bantam 70
 56
 57 (ix) FEATURE:
 58 (A) NAME/KEY: CDS
 59 (B) LOCATION: 46..4119
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 62 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
 63
 64 GTGCTGTGTT GTGCTGTGCT GCGTGCTGTG GAGGGGGAGG AGGAG ATG GGG AAG 54
 65 Met Gly Lys
 66 1
 67
 68 GAG GCA GGG GCA GCG GAG TCG TCG ACG GTG GTG CTG GCC GTC AAC GGC 102
 69 Glu Ala Gly Ala Ala Glu Ser Ser Thr Val Val Leu Ala Val Asn Gly
 70 5 10 15
 71
 72 AAG CGC TAC GAG GCG GCC GGC GTG GCT CCG TCC ACG TCG CTG CTG GAG 150
 73 Lys Arg Tyr Glu Ala Ala Gly Val Ala Pro Ser Thr Ser Leu Leu Glu
 74 20 25 30 35
 75
 76 TTC CTC CGC ACC CAG ACG CCC GTC AGA GGC CCC AAG CTC GGC TGC GGC 198
 77 Phe Leu Arg Thr Gln Thr Pro Val Arg Gly Pro Lys Leu Gly Cys Gly
 78 40 45 50
 79
 80 GAA GGT GGC TGC GGT GCA TGC GTG GTC CTC GTC TCC AAG TAC GAC CCG 246
 81 Glu Gly Gly Cys Gly Ala Cys Val Val Leu Val Ser Lys Tyr Asp Pro
 82 55 60 65
 83
 84 GCC ACG GAC GAG GTG ACC GAG TTC TCT GCC AGC TCC TGC CTG ACG CTG 294
 85 Ala Thr Asp Glu Val Thr Glu Phe Ser Ala Ser Ser Cys Leu Thr Leu
 86 70 75 80
 87
 88 CTC CAC AGC GTG GAC CGC TGC TCA GTG ACC ACC AGC GAG GGA ATC GGC 342
 89 Leu His Ser Val Asp Arg Cys Ser Val Thr Thr Ser Glu Gly Ile Gly
 90 85 90 95
 91
 92 AAC ACC AGG GAT GGC TAC CAC CCC GTG CAG CAG CGC CTC TCC GGC TTC 390
 93 Asn Thr Arg Asp Gly Tyr His Pro Val Gln Gln Arg Leu Ser Gly Phe
 94 100 105 110 115
 95
 96 CAC GCC TCG CAG TGC GGC TTC TGC ACA CCC GGC ATG TGC ATG TCC ATC 438
 97 His Ala Ser Gln Cys Gly Phe Cys Thr Pro Gly Met Cys Met Ser Ile
 98 120 125 130
 99

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100	TTC TCC GCC CTT GTC AAG GCC GAC AAC AAG TCC GAT CGC CCG GAC CCT	486
101	Phe Ser Ala Leu Val Lys Ala Asp Asn Lys Ser Asp Arg Pro Asp Pro	
102	135 140 145	
103		534
104	CCT GCT GGC TTC TCC AAG ATC ACT ACC TCG GAG GCA GAG AAG GCT GTC	
105	Pro Ala Gly Phe Ser Lys Ile Thr Thr Ser Glu Ala Glu Lys Ala Val	
106	150 155 160	
107		582
108	TCG GGC AAC CTT TGT CGT TGC ACC GGA TAC AGA CCC ATT GTT GAC ACC	
109	Ser Gly Asn Leu Cys Arg Cys Thr Gly Tyr Arg Pro Ile Val Asp Thr	
110	165 170 175	
111		630
112	TGC AAA AGC TTT GCC TCT GAT GTT GAC CTC GAG GAC CTA GGC CTC AAC	
113	Cys Lys Ser Phe Ala Ser Asp Val Asp Leu Glu Asp Leu Gly Leu Asn	
114	180 185 190 195	
115		678
116	TGT TTC TGG AAG AAG GGC GAA GAA CCT GCA GAA GTC AGC AGG CTG CCG	
117	Cys Phe Trp Lys Lys Gly Glu Glu Pro Ala Glu Val Ser Arg Leu Pro	
118	200 205 210	
119		726
120	GGG TAC AAC AGC GGT GCC GTC TGC ACC TTT CCA GAG TTT CTC AAA TCC	
121	Gly Tyr Asn Ser Gly Ala Val Cys Thr Phe Pro Glu Phe Leu Lys Ser	
122	215 220 225	
123		774
124	GAA ATC AAG TCT ACT ATG AAG CAG GTG AAC GAT GTC CCC ATT GCA GCC	
125	Glu Ile Lys Ser Thr Met Lys Gln Val Asn Asp Val Pro Ile Ala Ala	
126	230 235 240	
127		822
128	TCA GGT GAT GGC TGG TAC CAT CCT AAG AGC ATT GAA GAG CTT CAC AGG	
129	Ser Gly Asp Gly Trp Tyr His Pro Lys Ser Ile Glu Glu Leu His Arg	
130	245 250 255	
131		870
132	TTG TTT GAT TCC AGC TGG TTT GAT GAC AGT TCT GTG AAG ATT GTT GCT	
133	Leu Phe Asp Ser Ser Trp Phe Asp Asp Ser Ser Val Lys Ile Val Ala	
134	260 265 270 275	
135		918
136	TCA AAC ACT GGG TCT GGA GTG TAC AAG GAT CAG GAC CTC TAC GAC AAG	
137	Ser Asn Thr Gly Ser Gly Val Tyr Lys Asp Gln Asp Leu Tyr Asp Lys	
138	280 285 290	
139		966
140	TAC ATT GAC ATC AAA GGA ATC CCA GAG CTT TCA GTC ATC AAT AAA AAC	
141	Tyr Ile Asp Ile Lys Gly Ile Pro Glu Leu Ser Val Ile Asn Lys Asn	
142	295 300 305	
143		1014
144	GAC AAA GCA ATT GAG CTT GGA TCA GTT GTG TCC ATC TCT AAA GCT ATT	
145	Asp Lys Ala Ile Glu Leu Gly Ser Val Val Ser Ile Ser Lys Ala Ile	
146	310 315 320	
147		1062
148	GAA GTG CTG TCA GAT GGA AAT TTG GTC TTC AGA AAG ATT GCT GAT CAC	
149	Glu Val Leu Ser Asp Gly Asn Leu Val Phe Arg Lys Ile Ala Asp His	
150	325 330 335	
151		1110
152	CTC AAC AAA GTG GCT TCA CCG TTT GTT CGG AAC ACT GCA ACC ATA GGA	

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153	Leu Asn Lys Val Ala Ser Pro Phe Val Arg Asn Thr Ala Thr Ile Gly	355
154	340 345 350	
155		1158
156	GGA AAC ATA ATG ATG GCA CAA AGG TTG CCA TTT GAA TCG GAT GTT GCA	
157	Gly Asn Ile Met Met Ala Gln Arg Leu Pro Phe Glu Ser Asp Val Ala	
158	360 365 370	
159		1206
160	ACC GTG CTC CTA GCT GCG GGT TCG ACA GTC ACA GTC CAG GTG GCT TCC	
161	Thr Val Leu Leu Ala Ala Gly Ser Thr Val Thr Val Gln Val Ala Ser	
162	375 380 385	
163		1254
164	AAA AGG CTG TGC TTC ACT CTG GAG GAA TTC TTG GAA CAA CCT CCA TGT	
165	Lys Arg Leu Cys Phe Thr Leu Glu Glu Phe Leu Glu Gln Pro Pro Cys	
166	390 395 400	
167		1302
168	GAT TCT AGG ACC CTG CTG CTG AGC ATA TTT ATC CCA GAA TGG GGT TCA	
169	Asp Ser Arg Thr Leu Leu Leu Ser Ile Phe Ile Pro Glu Trp Gly Ser	
170	405 410 415	
171		1350
172	GAC TAT GTC ACC TTT GAG ACT TTC CGA GCC GCC CCA CGA CCA TTT GGA	
173	Asp Tyr Val Thr Phe Glu Thr Phe Arg Ala Ala Pro Arg Pro Phe Gly	
174	420 425 430 435	
175		1398
176	AAT GCT GTC TCT TAT GTA AAC TCT GCT TTC TTG GCA AGG ACA TCA GGC	
177	Asn Ala Val Ser Tyr Val Asn Ser Ala Phe Leu Ala Arg Thr Ser Gly	
178	440 445 450	
179		1446
180	AGC CTT CTA ATT GAG GAT ATA TGC TTG GCA TTT GGT GCC TAC GGA GTC	
181	Ser Leu Leu Ile Glu Asp Ile Cys Leu Ala Phe Gly Ala Tyr Gly Val	
182	455 460 465	
183		1494
184	GAT CAT GCC ATC AGA GCT AAG AAG GTT GAA GAT TTC TTG AAG GGA AAA	
185	Asp His Ala Ile Arg Ala Lys Lys Val Glu Asp Phe Leu Lys Gly Lys	
186	470 475 480	
187		1542
188	TCG CTG AGC TCA TTT GTG ATA CTT GAA GCA ATT AAA CTA CTC AAA GAT	
189	Ser Leu Ser Ser Phe Val Ile Leu Glu Ala Ile Lys Leu Leu Lys Asp	
190	485 490 495	
191		1590
192	ACC GTT TCA CCA TCA GAA GGC ACT ACA CAT CAT GAA TAC AGG GTC AGC	
193	Thr Val Ser Pro Ser Glu Gly Thr Thr His His Glu Tyr Arg Val Ser	
194	500 505 510 515	
195		1638
196	TTG GCT GTC AGT TTC TTG TTC AGT TTC TTA TCT TCC CTT GCC AAC AGT	
197	Leu Ala Val Ser Phe Leu Phe Ser Phe Leu Ser Ser Leu Ala Asn Ser	
198	520 525 530	
199		1686
200	TCG AGT GCA CCA TCA AAT ATT GAT ACT CCC AAT GGG TCA TAT ACT CAT	
201	Ser Ser Ala Pro Ser Asn Ile Asp Thr Pro Asn Gly Ser Tyr Thr His	
202	535 540 545	
203		1734
204	GAA ACT GGT AGC AAT GTG GAC TCA CCT GAG AGG CAT ATT AAG GTT GAC	
205	Glu Thr Gly Ser Asn Val Asp Ser Pro Glu Arg His Ile Lys Val Asp	

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	550	555	560	
206				
207				
208	AGC AAT GAT TTG CCA ATT CGT TCA AGA CAA GAA ATG GTT TTC AGC GAT			1782
209	Ser Asn Asp Leu Pro Ile Arg Ser Arg Gln Glu Met Val Phe Ser Asp			
210	565	570	575	
211				
212	GAG TAC AAG CCT GTT GGC AAG CCG ATC AAG AAA GTC GGG GCA GAG ATC			1830
213	Glu Tyr Lys Pro Val Gly Lys Pro Ile Lys Lys Val Gly Ala Glu Ile			
214	580	585	590	595
215				
216	CAA GCA TCA GGG GAG GCT GTG TAC GTT GAT GAT ATC CCT GCT CCC AAG			1878
217	Gln Ala Ser Gly Glu Ala Val Tyr Val Asp Asp Ile Pro Ala Pro Lys			
218		600	605	610
219				
220	GAT TGC CTC TAT GGA GCA TTT ATC TAC AGC ACA CAT CCT CAT GCT CAT			1926
221	Asp Cys Leu Tyr Gly Ala Phe Ile Tyr Ser Thr His Pro His Ala His			
222		615	620	625
223				
224	GTG AGA AGT ATC AAC TTC AAA TCA TCC TTG GCT TCA CAG AAG GTC ATC			1974
225	Val Arg Ser Ile Asn Phe Lys Ser Ser Leu Ala Ser Gln Lys Val Ile			
226		630	635	640
227				
228	ACA GTT ATA ACC GCA AAG GAT ATT CCA AGC GGT GGA GAA AAT ATT GGA			2022
229	Thr Val Ile Thr Ala Lys Asp Ile Pro Ser Gly Gly Glu Asn Ile Gly			
230		645	650	655
231				
232	AGC AGC TTC CTG ATG CAA GGA GAA GCA CTA TTT GCA GAT CCA ATC GCT			2070
233	Ser Ser Phe Leu Met Gln Gly Glu Ala Leu Phe Ala Asp Pro Ile Ala			
234	660	665	670	675
235				
236	GAA TTT GCT GGT CAA AAT ATT GGT GTC GTG ATT GCT GAA ACA CAA AGA			2118
237	Glu Phe Ala Gly Gln Asn Ile Gly Val Val Ile Ala Glu Thr Gln Arg			
238		680	685	690
239				
240	TAT GCT AAT ATG GCT GCA AAG CAA GCT GTT GTT GAG TAT AGC ACA GAA			2166
241	Tyr Ala Asn Met Ala Ala Lys Gln Ala Val Val Glu Tyr Ser Thr Glu			
242		695	700	705
243				
244	AAT CTG CAG CCA CCA ATT CTG ACA ATA GAA GAT GCC ATC CAA AGA AAC			2214
245	Asn Leu Gln Pro Pro Ile Leu Thr Ile Glu Asp Ala Ile Gln Arg Asn			
246		710	715	720
247				
248	AGC TAC ATC CAA ATT CCC CCA TTT TTA GCT CCA AAG CCA GTT GGT GAC			2262
249	Ser Tyr Ile Gln Ile Pro Pro Phe Leu Ala Pro Lys Pro Val Gly Asp			
250		725	730	735
251				
252	TAC AAC AAA GGG ATG GCT GAA GCA GAC CAC AAG ATT CTA TCA GCA GAG			2310
253	Tyr Asn Lys Gly Met Ala Glu Ala Asp His Lys Ile Leu Ser Ala Glu			
254	740	745	750	755
255				
256	GTA AAA CTT GAA TCC CAG TAC TAC TTC TAC ATG GAA ACT CAA GCA GCA			2358
257	Val Lys Leu Glu Ser Gln Tyr Tyr Phe Tyr Met Glu Thr Gln Ala Ala			
258		760	765	770

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